



## Molecular mechanisms of mastitis susceptibility in dairy cattles

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**Abstract:** Mastitis is one of the most costly diseases for dairy herds, which makes it among the major concerns for the dairy cattle industry [1]. *Escherichia coli* (*E. coli*) is a prevalent environmental pathogen that is characterized as a relatively short-term mastitis process and induces a distinct acute phase response [2]. However, significant evidence has shown that resistance to this disease has a genetic basis [3]. In the last decade, high-throughput genomic technologies such as high-density microarrays provide whole-genome approaches to address biological questions and facilitate our understanding of host-pathogen relations and provide mechanistic insight into the host resistance to mastitis [4]. In the current study, GSE24560 microarray data were used to investigate the physiological mechanisms involved in dairy cattle with different levels of susceptibility to mastitis with a focus on *E. coli* infection. The differentially expressed analysis of transcriptome profile, showed different responses to *E. coli* infection in the samples with favorable QTL allele (Q) compared to the unfavorable QTL allele (q), so that 328 up-regulated genes and 111 down-regulated genes in samples with Q in compare to 74 up-regulated genes and 26 down-regulated genes in q were introduced. Gene ontology (GO) analysis with biological process (BP) criterion revealed all enriched terms by up-regulated genes in q were covered by Q, including terms related to the immune system process, biological adhesion, and localization. Furthermore BP terms related to the main process including biological regulation, metabolic process, response to stimulus, signaling and etc. were enriched Specifically by up-regulated genes of Q. Interestingly down-regulated genes of q enriched three terms including hydrogen ion transmembrane transport, proton transport, and hydrogen transport which none of them appeared in GO terms related to Q. Whereas GO related to the main biological process such as cellular component organization, cellular metabolic process, positive regulation of biological process, positive regulation of cellular process and etc. were enriched by down-regulated genes of Q.

**Keywords:** Mastitis; Transcriptome; Microarray; Gene ontology; *Escherichia coli*

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